

SEQUENCE LISTING

<110> OLSON, ERIC
SPENCER, JEFFREY A.

<120> METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
IN STRIATED MUSCLE CELLS

<130> MYOG:028US

<140> UNKNOWN

<141> 2001-07-18

<150> 60/219,020

<151> 2000-07-18

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 1448

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (199)..(1296)

<400> 1

aaggagtgt a gacagagtgt ctggaaatag acaggggtga gaggagctgt taggggaagg 60

gacaggactc ttccaagagg gagcaatagc cggatccca agaatccagt cagcctaaac 120

tgaccgagga agggtgcaca ggcaggggag aaggccaacg acagggccac agcgaggcag 180

gctccagagc gccgcggg atg aac ttc acg gtg ggt ttc aag ccg ctg cta 231
Met Asn Phe Thr Val Gly Phe Lys Pro Leu Leu

1 5 10

ggg gat gcg cac aac atg gac aac ttg gag aag cag ctc att tgc ccc 279
Gly Asp Ala His Asn Met Asp Asn Leu Glu Lys Gln Leu Ile Cys Pro

15 20 25

atc tgc ctg gag atg ttc tcc aag ccc gtg gtg atc ttg ccc tgc caa 327
Ile Cys Leu Glu Met Phe Ser Lys Pro Val Val Ile Leu Pro Cys Gln

30 35 40

cac aac ctg tgc cgc aag tgt gcc aac gac gtc ttc cag gcc tct aat 375
His Asn Leu Cys Arg Lys Cys Ala Asn Asp Val Phe Gln Ala Ser Asn

45 50 55

cct ctg tgg caa tcc cgg ggc tcc aca acg gtg tct tca gga gga cgt 423
Pro Leu Trp Gln Ser Arg Gly Ser Thr Thr Val Ser Ser Gly Gly Arg

60 65 70 75

ttc cga tgc cca tct tgt agg cac gag gtt gtc ctg gac agg cat ggt 471

Phe	Arg	Cys	Pro	Ser	Cys	Arg	His	Glu	Val	Val	Leu	Asp	Arg	His	Gly		
									80		85				90		
gtc	tat	ggc	ctg	cag	cg	aac	ctg	cta	gtg	gag	aac	atc	att	gac	atc	519	
Val	Tyr	Gly	Leu	Gln	Arg	Asn	Leu	Leu	Val	Glu	Asn	Ile	Ile	Asp	Ile		
									95		100				105		
tac	aag	cag	gag	tcc	tcc	cg	cca	ctg	cac	gcc	aag	gt	gaa	cag	cac	567	
Tyr	Lys	Gln	Glu	Ser	Ser	Arg	Pro	Leu	His	Ala	Lys	Ala	Glu	Gln	His		
									110		115				120		
ctc	atg	tgt	gag	gag	cac	gag	gac	gag	aag	atc	aac	atc	ta	c	tg	615	
Leu	Met	Cys	Glu	Glu	His	Glu	Asp	Glu	Lys	Ile	Asn	Ile	Tyr	Cys	Leu		
									125		130				135		
agc	tgc	gag	gt	ccc	acc	tgc	tct	ctc	tgc	aag	gtt	ttc	ggc	gcc	cac	663	
Ser	Cys	Glu	Val	Pro	Thr	Cys	Ser	Leu	Cys	Lys	Val	Phe	Gly	Ala	His		
									140		145				155		
aag	gac	tgt	gag	gt	gcc	cct	ctg	ccc	acc	att	ta	aaa	cgc	cag	aag	711	
Lys	Asp	Cys	Glu	Val	Ala	Pro	Leu	Pro	Thr	Ile	Tyr	Lys	Arg	Gln	Lys		
									160		165				170		
agt	gag	ctg	agc	gat	ggc	atc	g	atg	ctg	gt	g	gc	gg	aat	gac	cgt	759
Ser	Glu	Leu	Ser	Asp	Gly	Ile	Ala	Met	Leu	Val	Ala	Gly	Asn	Asp	Arg		
									175		180				185		
gt	g	ca	gt	atc	ac	cag	atg	gag	gt	tg	cag	ac	cc	att	gag	807	
Val	Gln	Ala	Val	Ile	Thr	Gln	Met	Glu	Glu	Val	Cys	Gln	Thr	Ile	Glu		
									190		195				200		
gac	aac	agc	cgc	aga	cag	aag	caa	ctg	tta	aa	cag	agg	ttc	gag	acc	855	
Asp	Asn	Ser	Arg	Arg	Gln	Lys	Gln	Leu	Leu	Asn	Gln	Arg	Phe	Glu	Thr		
									205		210				215		
ctg	tgc	g	cg	gtt	ttg	gag	gag	cg	aag	gg	ctg	ctt	caa	gca	ctg	903	
Leu	Cys	Ala	Val	Leu	Glu	Glu	Arg	Lys	Gly	Glu	Leu	Leu	Gln	Ala	Leu		
									220		225				235		
gcc	cg	g	ag	cag	gag	aag	ttg	cag	cg	gt	cg	gg	gc	ct	atc	cgc	951
Ala	Arg	Glu	Gln	Glu	Lys	Leu	Gln	Arg	Val	Arg	Gly	Leu	Ile	Arg			
									240		245				250		
cag	ta	g	ga	gac	ca	ttg	gag	gg	tcc	tca	aag	ctg	gt	gag	tcc	gg	999
Gln	Tyr	Gly	Asp	His	Leu	Glu	Gly	Ser	Ser	Lys	Leu	Val	Glu	Ser	Ala		
										255		260			265		
atc	cag	tcc	atg	gag	gag	ccg	cag	atg	g	ct	tc	c	cag	cag	gca	1047	
Ile	Gln	Ser	Met	Glu	Glu	Pro	Gln	Met	Ala	Leu	Tyr	Leu	Gln	Gln	Ala		
									270		275				280		
aag	gag	ctg	atc	aac	aag	gtc	gg	gg	gca	atg	tcg	aag	gt	gag	ctg	gca	1095
Lys	Glu	Leu	Ile	Asn	Lys	Val	Gly	Ala	Met	Ser	Lys	Val	Glu	Leu	Ala		
									285		290				295		
gga	cg	cg	gag	cc	gg	tc	at	g	ag	ca	tt	tc	tc	tg	ag	gc	1143
Gly	Arg	Pro	Glu	Pro	Gly	Tyr	Glu	Ser	Met	Glu	Gln	Phe	Ser	Val	Ser		

300	305	310	315	
gtg gag cac gtg gcc gaa atg ttg cga acc atc gac ttc cag ccg ggc Val Glu His Val Ala Glu Met Leu Arg Thr Ile Asp Phe Gln Pro Gly				1191
320		325	330	
gcc gct ggg gat gaa gag gat gac gac atg gct ttg gat ggg gag gag Ala Ala Gly Asp Glu Glu Asp Asp Met Ala Leu Asp Gly Glu Glu				1239
335	340		345	
ggc aat gcg ggg ctg gag gag cggtt gac gtg cca gaa ggc tca Gly Asn Ala Gly Leu Glu Glu Arg Leu Asp Val Pro Glu Gly Ser				1287
350	355		360	
ggc ctg cac tgacccgact ctgatccaga gcgcacacccc gaagcgggag Gly Leu His				1336
365				
ccaagggatg ctgaggatct gcgcagagac caccgcgcca ccaagctcggtttccccc ccggaaaggt tctcaataaa ggactcaagt gtccc				1396
				1434

MUS MUSCULUS PROTEIN

<210> 2
<211> 366
<212> PRT
<213> Mus musculus

<400> 2
Met Asn Phe Thr Val Gly Phe Lys Pro Leu Leu Gly Asp Ala His Asn
1 5 10 15

Met Asp Asn Leu Glu Lys Gln Leu Ile Cys Pro Ile Cys Leu Glu Met
20 25 30

Phe Ser Lys Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys Arg
35 40 45

Lys Cys Ala Asn Asp Val Phe Gln Ala Ser Asn Pro Leu Trp Gln Ser
50 55 60

Arg Gly Ser Thr Thr Val Ser Ser Gly Gly Arg Phe Arg Cys Pro Ser
65 70 75 80

Cys Arg His Glu Val Val Leu Asp Arg His Gly Val Tyr Gly Leu Gln
85 90 95

Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu Ser
100 105 110

Ser Arg Pro Leu His Ala Lys Ala Glu Gln His Leu Met Cys Glu Glu
115 120 125

His Glu Asp Glu Lys Ile Asn Ile Tyr Cys Leu Ser Cys Glu Val Pro
130 135 140

Thr Cys Ser Leu Cys Lys Val Phe Gly Ala His Lys Asp Cys Glu Val

145	150	155	160
Ala Pro Leu Pro Thr Ile Tyr Lys Arg Gln Lys Ser Glu Leu Ser Asp			
165		170	175
Gly Ile Ala Met Leu Val Ala Gly Asn Asp Arg Val Gln Ala Val Ile			
180	185		190
Thr Gln Met Glu Glu Val Cys Gln Thr Ile Glu Asp Asn Ser Arg Arg			
195	200		205
Gln Lys Gln Leu Leu Asn Gln Arg Phe Glu Thr Leu Cys Ala Val Leu			
210	215		220
Glu Glu Arg Lys Gly Glu Leu Leu Gln Ala Leu Ala Arg Glu Gln Glu			
225	230	235	240
Glu Lys Leu Gln Arg Val Arg Gly Leu Ile Arg Gln Tyr Gly Asp His			
245		250	255
Leu Glu Gly Ser Ser Lys Leu Val Glu Ser Ala Ile Gln Ser Met Glu			
260	265		270
Glu Pro Gln Met Ala Leu Tyr Leu Gln Gln Ala Lys Glu Leu Ile Asn			
275	280		285
Lys Val Gly Ala Met Ser Lys Val Glu Leu Ala Gly Arg Pro Glu Pro			
290	295		300
Gly Tyr Glu Ser Met Glu Gln Phe Ser Val Ser Val Glu His Val Ala			
305	310	315	320
Glu Met Leu Arg Thr Ile Asp Phe Gln Pro Gly Ala Ala Gly Asp Glu			
325	330		335
Glu Asp Asp Asp Met Ala Leu Asp Gly Glu Glu Gly Asn Ala Gly Leu			
340	345		350
Glu Glu Glu Arg Leu Asp Val Pro Glu Gly Ser Gly Leu His			
355	360		365

<210> 3
 <211> 2590
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (80)..(1714)

<400> 3
 ctcgagattt acccttacag aagctgttcg ggagcacctt tcccttggca gcacactcag 60
 ggcacaggac ggcaaggaa atg agc act tct ctg aat tac aag tct ttc tcc 112
 Met Ser Thr Ser Leu Asn Tyr Lys Ser Phe Ser

1	5	10	
aaa gag cag cag acc atg gat aac ttg gaa aag caa ctg atc tgt ccc Lys Glu Gln Gln Thr Met Asp Asn Leu Glu Lys Gln Leu Ile Cys Pro	15	20	160
		25	
atc tgc cta gag atg ttc acg aag cct gtg gtc att ctc cct tgc cag Ile Cys Leu Glu Met Phe Thr Lys Pro Val Val Ile Leu Pro Cys Gln	30	35	208
		40	
cac aac ctg tgc agg aaa tgt gcc agt gac atc ttc cag gcc tct aac His Asn Leu Cys Arg Lys Cys Ala Ser Asp Ile Phe Gln Ala Ser Asn	45	50	256
		55	
ccg tac tta ccc aca aga gga ggc acc acc gtg gca tca ggg ggc cgc Pro Tyr Leu Pro Thr Arg Gly Gly Thr Thr Val Ala Ser Gly Gly Arg	60	65	304
		70	
ttc cgc tgt ccc tcc tgc aga cat gag gtg gtg tta gac aga cat ggg Phe Arg Cys Pro Ser Cys Arg His Glu Val Val Leu Asp Arg His Gly	80	85	352
		90	
gtc tat gga ctg cag agg aac ctg ctc gtg gaa aac att att gat atc Val Tyr Gly Leu Gln Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile	95	100	400
		105	
tac aag cag gaa tcc acc agg cca gaa aaa aaa ttg gac cag ccc atg Tyr Lys Gln Glu Ser Thr Arg Pro Glu Lys Lys Leu Asp Gln Pro Met	110	115	448
		120	
tgt gaa gag cat gaa gag gaa cgc atc aac atc tat tgt ctg aac tgt Cys Glu Glu His Glu Glu Arg Ile Asn Ile Tyr Cys Leu Asn Cys	125	130	496
		135	
gaa gtg ccc acc tgt tcc ttg tgc aag gtt ttt ggc gcc cat aag gac Glu Val Pro Thr Cys Ser Leu Cys Lys Val Phe Gly Ala His Lys Asp	140	145	544
		150	
		155	
tgc cag gtg gct ccc ctg act cat gtg ttc cag agg cag aag tca gag Cys Gln Val Ala Pro Leu Thr His Val Phe Gln Arg Gln Lys Ser Glu	160	165	592
		170	
ctc agt gat ggt att gct gta ctt gtg gga agc aac gat aga gtc cag Leu Ser Asp Gly Ile Ala Val Leu Val Gly Ser Asn Asp Arg Val Gln	175	180	640
		185	
ggt gtg atc agc cag ctg gag gac acc tgt aaa act att gag gag tgc Gly Val Ile Ser Gln Leu Glu Asp Thr Cys Lys Thr Ile Glu Glu Cys	190	195	688
		200	
tgc aga aag cag aaa cag gac ctg tgt gag aaa ttt gat cac cta tac Cys Arg Lys Gln Lys Gln Asp Leu Cys Glu Lys Phe Asp His Leu Tyr	205	210	736
		215	
ggc atc ctg gag gag agg aag act gaa atg acc caa gcc atc act cga Gly Ile Leu Glu Glu Arg Lys Thr Glu Met Thr Gln Ala Ile Thr Arg	220	225	784
		230	
		235	

aca cag gag gag aaa ctg gaa cat gtc cga act ctt atc agg aag tat		832	
Thr Gln Glu Glu Lys Leu Glu His Val Arg Thr Leu Ile Arg Lys Tyr			
240	245	250	
tcc gat cac ctg gag aac gta tcc aag ttg gtg gag tca gga atc cag		880	
Ser Asp His Leu Glu Asn Val Ser Lys Leu Val Glu Ser Gly Ile Gln			
255	260	265	
ttc atg gat gag ccc gaa atg gca gta ttt ctg cag aat gcc aag acc		928	
Phe Met Asp Glu Pro Glu Met Ala Val Phe Leu Gln Asn Ala Lys Thr			
270	275	280	
ctg ttg caa aag atc gtg gaa gca tca aag gcg ttt cag atg gag aaa		976	
Leu Leu Gln Lys Ile Val Glu Ala Ser Lys Ala Phe Gln Met Glu Lys			
285	290	295	
cta gaa caa ggt tat gag atc atg agc aac ttc act gtc aat ctc aat		1024	
Leu Glu Gln Gly Tyr Glu Ile Met Ser Asn Phe Thr Val Asn Leu Asn			
300	305	310	315
aga gaa gaa aaa att atc cgt gaa att gac ttt tct aga gaa gag gaa		1072	
Arg Glu Glu Lys Ile Ile Arg Glu Ile Asp Phe Ser Arg Glu Glu Glu			
320	325	330	
gag gaa gaa gat gca gga gaa ata gat gaa gaa gga gaa gga gag gat		1120	
Glu Glu Glu Asp Ala Gly Glu Ile Asp Glu Glu Gly Glu Gly Glu Asp			
335	340	345	
gca gta gaa gta gaa gag gca gaa aat gtt caa ata gca tct tca ggg		1168	
Ala Val Glu Val Glu Ala Glu Asn Val Gln Ile Ala Ser Ser Gly			
350	355	360	
gaa gag gag agt ctg gag aaa gct gca gag ccc tct cag ctt ccc gca		1216	
Glu Glu Glu Ser Leu Glu Lys Ala Ala Glu Pro Ser Gln Leu Pro Ala			
365	370	375	
gag ctt cag gtc gcc cca gag cca cta cct gct tcc tct cca gaa ccg		1264	
Glu Leu Gln Val Ala Pro Glu Pro Leu Pro Ala Ser Ser Pro Glu Pro			
380	385	390	395
ttt tca tcc atg cca cct gct gca gat gtc ctg gtg aca cag ggg gag		1312	
Phe Ser Ser Met Pro Pro Ala Ala Asp Val Leu Val Thr Gln Gly Glu			
400	405	410	
gtg gtg ccc att ggc tct cag cag acc aca cag tct gaa act tca ggc		1360	
Val Val Pro Ile Gly Ser Gln Gln Thr Thr Gln Ser Glu Thr Ser Gly			
415	420	425	
cct tca gca gcg gaa act gcg gat ccc ttg ttt tac cct agt tgg tat		1408	
Pro Ser Ala Ala Glu Thr Ala Asp Pro Leu Phe Tyr Pro Ser Trp Tyr			
430	435	440	
aaa ggc caa agc cgg aaa acc agc tcc aac cca cct tgc act cat ggg		1456	
Lys Gly Gln Ser Arg Lys Thr Ser Ser Asn Pro Pro Cys Thr His Gly			
445	450	455	

agt gaa ggt ctg ggt caa ata ggg cct ctg ggc att gag gat tcc agt		1504	
Ser Glu Gly Leu Gly Gln Ile Gly Pro Leu Gly Ile Glu Asp Ser Ser			
460	465	470	475
gtg cag tcc gca gaa gtg gca gaa gcc gca acc aat gag cag gca gca		1552	
Val Gln Ser Ala Glu Val Ala Ala Thr Asn Glu Gln Ala Ala			
480	485	490	
gtg agt ggt aag gag tct agt tca act gca gct acc tct cag att gga		1600	
Val Ser Gly Lys Glu Ser Ser Thr Ala Ala Thr Ser Gln Ile Gly			
495	500	505	
ttt gag gcc cct tct ccc cag gga cag tct gca gcc ttg ggg agt ggg		1648	
Phe Glu Ala Pro Ser Pro Gln Gly Gln Ser Ala Ala Leu Gly Ser Gly			
510	515	520	
ggg ggt atc ctg agc cag ctc gcc acg tct tct cct tct cct ggt		1696	
Gly Gly Val Ile Leu Ser Gln Leu Ala Thr Ser Ser Pro Ser Pro Gly			
525	530	535	
ttg aat tcc cta aat gaa taatatttat ttcgttgct gccccctgtc		1744	
Leu Asn Ser Leu Asn Glu			
540	545		
tgcctggctg aaaaggcacat aggcagcagg aaacaggtgg aaattcacca cgattcatat		1804	
gaaggggacc tctggacagg atttctgaaa gcaaaacaaa acaatacaac accaccaccc		1864	
tttaattcca gatgacttat ctcactcatt gagaaaatga ttatgctcag aacaaaatta		1924	
cagaaaatac tcttctgaag aaacttgatc ttctgcaaatt ctttcatttg tgtgagaac		1984	
cttctgaagg ttgtgttaggt gtggtgcatg cctgtgtatc agccataagt gccaagtgg		2044	
aacaaagtgg cagaacactc tcccagcctc ctcaggctt ctggttattt taggacgctt		2104	
gtgccttttg ctttctcct tagcattgca ggtggtaggt gatgttcagt gtcagttcca		2164	
aactgaccga tttatcaaaa tatggagatt ggtcaactgac caaagctatg tagggcactg		2224	
tagaggttcc tttccctatg gatgccatgg gtgcgcagac aggacttcc tttacatgtg		2284	
gccacacgtc catagtccag aaggccaaaa atctaggca actctttga cattttcta		2344	
accttattta catatctcat aatcatatcc atgtatttagg catttaatt gaatttcaaa		2404	
gaggagctgt ctactttctt aagtgtcctg ccatagcagc aatctgataa tctgtggagc		2464	
aactgcatgg atttaagtat acacacaatt ctccccctgt gtgccttc tctctcttc		2524	
tctccccctc tctccctctg tctcttc tccccctctgt ctctccctcc tttcctttct		2584	
tcctcc		2590	

<210> 4
<211> 545

<212> PRT

<213> Mus musculus

<400> 4

Met Ser Thr Ser Leu Asn Tyr Lys Ser Phe Ser Lys Glu Gln Gln Thr
1 5 10 15

Met Asp Asn Leu Glu Lys Gln Leu Ile Cys Pro Ile Cys Leu Glu Met
20 25 30

Phe Thr Lys Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys Arg
35 40 45

Lys Cys Ala Ser Asp Ile Phe Gln Ala Ser Asn Pro Tyr Leu Pro Thr
50 55 60

Arg Gly Gly Thr Thr Val Ala Ser Gly Gly Arg Phe Arg Cys Pro Ser
65 70 75 80

Cys Arg His Glu Val Val Leu Asp Arg His Gly Val Tyr Gly Leu Gln
85 90 95

Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu Ser
100 105 110

Thr Arg Pro Glu Lys Lys Leu Asp Gln Pro Met Cys Glu Glu His Glu
115 120 125

Glu Glu Arg Ile Asn Ile Tyr Cys Leu Asn Cys Glu Val Pro Thr Cys
130 135 140

Ser Leu Cys Lys Val Phe Gly Ala His Lys Asp Cys Gln Val Ala Pro
145 150 155 160

Leu Thr His Val Phe Gln Arg Gln Lys Ser Glu Leu Ser Asp Gly Ile
165 170 175

Ala Val Leu Val Gly Ser Asn Asp Arg Val Gln Gly Val Ile Ser Gln
180 185 190

Leu Glu Asp Thr Cys Lys Thr Ile Glu Glu Cys Cys Arg Lys Gln Lys
195 200 205

Gln Asp Leu Cys Glu Lys Phe Asp His Leu Tyr Gly Ile Leu Glu Glu
210 215 220

Arg Lys Thr Glu Met Thr Gln Ala Ile Thr Arg Thr Gln Glu Glu Lys
225 230 235 240

Leu Glu His Val Arg Thr Leu Ile Arg Lys Tyr Ser Asp His Leu Glu
245 250 255

Asn Val Ser Lys Leu Val Glu Ser Gly Ile Gln Phe Met Asp Glu Pro
260 265 270

Glu Met Ala Val Phe Leu Gln Asn Ala Lys Thr Leu Leu Gln Lys Ile
275 280 285

Val Glu Ala Ser Lys Ala Phe Gln Met Glu Lys Leu Glu Gln Gly Tyr
 290 295 300
 Glu Ile Met Ser Asn Phe Thr Val Asn Leu Asn Arg Glu Glu Lys Ile
 305 310 315 320
 Ile Arg Glu Ile Asp Phe Ser Arg Glu Glu Glu Glu Asp Ala
 325 330 335
 Gly Glu Ile Asp Glu Glu Gly Glu Asp Ala Val Glu Val Glu
 340 345 350
 Glu Ala Glu Asn Val Gln Ile Ala Ser Ser Gly Glu Glu Ser Leu
 355 360 365
 Glu Lys Ala Ala Glu Pro Ser Gln Leu Pro Ala Glu Leu Gln Val Ala
 370 375 380
 Pro Glu Pro Leu Pro Ala Ser Ser Pro Glu Pro Phe Ser Ser Met Pro
 385 390 395 400
 Pro Ala Ala Asp Val Leu Val Thr Gln Gly Glu Val Val Pro Ile Gly
 405 410 415
 Ser Gln Gln Thr Thr Gln Ser Glu Thr Ser Gly Pro Ser Ala Ala Glu
 420 425 430
 Thr Ala Asp Pro Leu Phe Tyr Pro Ser Trp Tyr Lys Gly Gln Ser Arg
 435 440 445
 Lys Thr Ser Ser Asn Pro Pro Cys Thr His Gly Ser Glu Gly Leu Gly
 450 455 460
 Gln Ile Gly Pro Leu Gly Ile Glu Asp Ser Ser Val Gln Ser Ala Glu
 465 470 475 480
 Val Ala Glu Ala Ala Thr Asn Glu Gln Ala Ala Val Ser Gly Lys Glu
 485 490 495
 Ser Ser Ser Thr Ala Ala Thr Ser Gln Ile Gly Phe Glu Ala Pro Ser
 500 505 510
 Pro Gln Gly Gln Ser Ala Ala Leu Gly Ser Gly Gly Val Ile Leu
 515 520 525
 Ser Gln Leu Ala Thr Ser Ser Pro Ser Pro Gly Leu Asn Ser Leu Asn
 530 535 540
 Glu
 545

<210> 5
 <211> 1597
 <212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (299)..(1327)

<400> 5

ctcgagattt acccttacag aagctgttcg ggagcacctt tcccttggca gcacactcag 60

ggacagggac ggcaaggaaa tgagcacttc tctgaattac aagtctttct ccaaagagca 120

gcagaccatg gataacttgg aaaagcaact gatctgtccc atctgcctag agatgttcac 180

gaagcctgtg gtcattctcc cttgccagca caacctgtgc aggaaatgtg cggggcccccc 240

ttggagacaa agacttggtg tgacgcaggt gggcaagaca gtcgcatttc aaagcaat 298

atg gat tat aaa tct agc ctg att cct gat gga aac gct atg gag aac 346

Met Asp Tyr Lys Ser Ser Leu Ile Pro Asp Gly Asn Ala Met Glu Asn

1

5

10

15

ctg gag aag cag ctg atc tgc ccc atc tgc ctg gag atg ttt acc aag 394

Leu Glu Lys Gln Leu Ile Cys Pro Ile Cys Leu Glu Met Phe Thr Lys

20

25

30

cct gtg gtc atc ctg ccc tgc caa cac aac ctc tgc cggt aag tgt gcc 442

Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys Arg Lys Cys Ala

35

40

45

aac gac atc ttc cag gct gcg aat ccc tac tgg acc aac cgc ggt ggc 490

Asn Asp Ile Phe Gln Ala Ala Asn Pro Tyr Trp Thr Asn Arg Gly Gly

50

55

60

tca gtg tcc atg tct gga ggt cgt ttc cgt tgc ccc tcg tgc cgc cat 538

Ser Val Ser Met Ser Gly Gly Arg Phe Arg Cys Pro Ser Cys Arg His

65

70

75

80

gaa gtg atc atg gac cgg cac ggg gtg tac ggc ctg cag agg aac ctg 586

Glu Val Ile Met Asp Arg His Gly Val Tyr Gly Leu Gln Arg Asn Leu

85

90

95

ctg gtg gaa aac atc att gac atc tac aag cag gag tgc tcc agt cggt 634

Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu Cys Ser Ser Arg

100

105

110

ccc ctg cag aaa ggc agc cac ccg atg tgc aag gaa cac gaa gac gag 682

Pro Leu Gln Lys Gly Ser His Pro Met Cys Lys Glu His Glu Asp Glu

115

120

125

aag atc aac atc tac tgt ctc acg tgt gag gtg cct act tgc tcc ttg 730

Lys Ile Asn Ile Tyr Cys Leu Thr Cys Glu Val Pro Thr Cys Ser Leu

130

135

140

tgc aag gtg ttt ggg gct cac cag gcc tgt gag gtt gcc cct ttg caa 778

Cys Lys Val Phe Gly Ala His Gln Ala Cys Glu Val Ala Pro Leu Gln

145

150

155

160

agc atc ttc caa gga cag aag act gag ctg agt aac tgc atc tcc atg Ser Ile Phe Gln Gly Gln Lys Thr Glu Leu Ser Asn Cys Ile Ser Met	165	170	175	826
ctg gtg gcg ggg aac gac cga gtg cag acg atc atc tct cag ctg gag Leu Val Ala Gly Asn Asp Arg Val Gln Thr Ile Ile Ser Gln Leu Glu	180	185	190	874
gac tcg tgc aga gtg acc aag gag aat agc cac cag gtg aag gag gag Asp Ser Cys Arg Val Thr Lys Glu Asn Ser His Gln Val Lys Glu Glu	195	200	205	922
ctg agt cag aag ttt gac acc ctc tac gcc atc ctg gat gag aag aag Leu Ser Gln Lys Phe Asp Thr Leu Tyr Ala Ile Leu Asp Glu Lys Lys	210	215	220	970
agc gag ctg ctg cag cgg atc acg cag gag cag gag aag ctg ggc Ser Glu Leu Leu Gln Arg Ile Thr Gln Glu Gln Glu Lys Leu Gly	225	230	235	240
ttc atc gag gct ctg atc ctc cag tac agg gag cag ctg gaa aag tcc Phe Ile Glu Ala Leu Ile Leu Gln Tyr Arg Glu Gln Leu Glu Lys Ser	245	250	255	1066
acc aag ctt gtg gag acc gcc atc cag tcc ctg gat gag ccc gga ggg Thr Lys Leu Val Glu Thr Ala Ile Gln Ser Leu Asp Glu Pro Gly Gly	260	265	270	1114
gct acc ttc ctc tca agt gcc aag cag ctc atc aag agc att gta gaa Ala Thr Phe Leu Ser Ser Ala Lys Gln Leu Ile Lys Ser Ile Val Glu	275	280	285	1162
gcc tcc aag ggc tgc cag ctg ggg aag aca gag caa ggc ttt gag aac Ala Ser Lys Gly Cys Gln Leu Gly Lys Thr Glu Gln Gly Phe Glu Asn	290	295	300	1210
atg gac tac ttt act ctg gac tta gaa cac ata gca gag gcc ttg agg Met Asp Tyr Phe Thr Leu Asp Leu Glu His Ile Ala Glu Ala Leu Arg	305	310	315	320
gcc att gac ttt ggg aca ggt aaa gga tgt gat gtt aca tgt ttg acc Ala Ile Asp Phe Gly Thr Gly Lys Gly Cys Asp Val Thr Cys Leu Thr	325	330	335	1306
ttt gaa agg cag cgt tcc tct tgagttctga ggggaactgt taaaaaagt Phe Glu Arg Gln Arg Ser Ser	340			1357
aaatttacac agccagtgtt gacaggtctc tctatggagc cctgactgtc ttagtagtgt 1417				
ctaagtagac caagctggtc tggAACACAT agagatctat cttgccccatc tctgcttctt 1477				
gagggatgag ataaaaggca tgtgccacc atgcctggct ccacagacaa ctttgtatg 1537				
gatccagggc ctggcacagt gcctggtaca taattgttgc gaaataaatt atctcggtcc 1597				

<210> 6
<211> 343
<212> PRT
<213> Mus musculus

<400> 6
Met Asp Tyr Lys Ser Ser Leu Ile Pro Asp Gly Asn Ala Met Glu Asn
1 5 10 15
Leu Glu Lys Gln Leu Ile Cys Pro Ile Cys Leu Glu Met Phe Thr Lys
20 25 30
Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys Arg Lys Cys Ala
35 40 45
Asn Asp Ile Phe Gln Ala Ala Asn Pro Tyr Trp Thr Asn Arg Gly Gly
50 55 60
Ser Val Ser Met Ser Gly Gly Arg Phe Arg Cys Pro Ser Cys Arg His
65 70 75 80
Glu Val Ile Met Asp Arg His Gly Val Tyr Gly Leu Gln Arg Asn Leu
85 90 95
Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu Cys Ser Ser Arg
100 105 110
Pro Leu Gln Lys Gly Ser His Pro Met Cys Lys Glu His Glu Asp Glu
115 120 125
Lys Ile Asn Ile Tyr Cys Leu Thr Cys Glu Val Pro Thr Cys Ser Leu
130 135 140
Cys Lys Val Phe Gly Ala His Gln Ala Cys Glu Val Ala Pro Leu Gln
145 150 155 160
Ser Ile Phe Gln Gly Gln Lys Thr Glu Leu Ser Asn Cys Ile Ser Met
165 170 175
Leu Val Ala Gly Asn Asp Arg Val Gln Thr Ile Ile Ser Gln Leu Glu
180 185 190
Asp Ser Cys Arg Val Thr Lys Glu Asn Ser His Gln Val Lys Glu Glu
195 200 205
Leu Ser Gln Lys Phe Asp Thr Leu Tyr Ala Ile Leu Asp Glu Lys Lys
210 215 220
Ser Glu Leu Leu Gln Arg Ile Thr Gln Glu Gln Glu Lys Leu Gly
225 230 235 240
Phe Ile Glu Ala Leu Ile Leu Gln Tyr Arg Glu Gln Leu Glu Lys Ser
245 250 255
Thr Lys Leu Val Glu Thr Ala Ile Gln Ser Leu Asp Glu Pro Gly Gly
260 265 270

Ala Thr Phe Leu Ser Ser Ala Lys Gln Leu Ile Lys Ser Ile Val Glu
275 280 285

Ala Ser Lys Gly Cys Gln Leu Gly Lys Thr Glu Gln Gly Phe Glu Asn
290 295 300

Met Asp Tyr Phe Thr Leu Asp Leu Glu His Ile Ala Glu Ala Leu Arg
305 310 315 320

Ala Ile Asp Phe Gly Thr Gly Lys Gly Cys Asp Val Thr Cys Leu Thr
325 330 335

Phe Glu Arg Gln Arg Ser Ser
340

WPS Office - Microsoft Word Document